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RAW SEQUENCE LISTING DATE: 07/02/2002 PATENT APPLICATION: US/10/081,806 TIME: 14:00:32

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## SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
             (i) APPLICANT: Prudent, James R.
                            Hall, Jeff G.
     6
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                            Lyamichev, Victor I.
            (ii) TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids
     9
           (iii) NUMBER OF SEQUENCES: 69
     11
            (iv) CORRESPONDENCE ADDRESS:
    13
                  (A) ADDRESSEE: Medlen & Carroll, LLP
     14
                  (B) STREET: 220 Montgomery Street, Suite 2200
     15
                                                           ENTERED
                  (C) CITY: San Francisco
     17
                  (D) STATE: California
                  (E) COUNTRY: United States Of America
     18
                  (F) ZIP: 94104
     19
     21
             (V) COMPUTER READABLE FORM:
                  (A) MEDIUM TYPE: Floppy disk
     22
                  (B) COMPUTER: IBM PC compatible
     23
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     24
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     25
            (vi) CURRENT APPLICATION DATA:
     27
                  (A) APPLICATION NUMBER: US/10/081,806
C--> 28
                  (B) FILING DATE: 22-Feb-2002
C--> 29
     30
                  (C) CLASSIFICATION:
           (vii) PRIOR APPLICATION DATA:
     40
                  (A) APPLICATION NUMBER: US/08/756,386
     33
                  (B) FILING DATE:
     34
                  (A) APPLICATION NUMBER: US 08/682,853
     37
                  (B) FILING DATE: 12-JUL-1996
     38
                  (A) APPLICATION NUMBER: US 08/599,491
     41
                  (B) FILING DATE: 24-JAN-1996
     42
     44
          (viii) ATTORNEY/AGENT INFORMATION:
                  (A) NAME: Ingolia, Diane E.
     45
                  (B) REGISTRATION NUMBER: 40,027
     46
     47
                  (C) REFERENCE/DOCKET NUMBER: FORS-02564
     49
            (ix) TELECOMMUNICATION INFORMATION:
                  (A) TELEPHONE: (415) 705-8410
     50
                  (B) TELEFAX: (415) 397-8338
     51
        (2) INFORMATION FOR SEQ ID NO: 1:
     54
             (i) SEQUENCE CHARACTERISTICS:
     56
                  (A) LENGTH: 2506 base pairs
     57
     58
                  (B) TYPE: nucleic acid
     59
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear
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(ii) MOLECULE TYPE: DNA (genomic)
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       (xi) SEQUENCE DESCRIPTION: SEO ID NO: 1:
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72 GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC
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76 TACAAGGCGG GCCGGGCCCC CACGCCGGAG GACTTTCCCC GGCAACTCGC CCTCATCAAG
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82 GCCGACAAAG ACCTTTACCA GCTCCTTTCC GACCGCATCC ACGTCCTCCA CCCCGAGGGG
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84 TACCTCATCA CCCCGGCCTG GCTTTGGGAA AAGTACGGCC TGAGGCCCGA CCAGTGGGCC
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102 GCCCTCAGGG ACCTGAAGGA GGCGCGGGGG CTTCTCGCCA AAGACCTGAG CGTTCTGGCC
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104 CTGAGGGAAG GCCTTGGCCT CCCGCCCGGC GACGACCCCA TGCTCCTCGC CTACCTCCTG
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134 GCGGCCAAGA CCATCAACTT CGGGGTCCTC TACGGCATGT CGGCCCACCG CCTCTCCCAG
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136 GAGCTAGCCA TCCCTTACGA GGAGGCCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC
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138 CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG
140 GAGACCCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT GAAGAGCGTG
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144 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC
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148 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCT GGAGGTGGAG
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152 (2) INFORMATION FOR SEQ ID NO: 2:
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         (i) SEQUENCE CHARACTERISTICS:
155
              (A) LENGTH: 2496 base pairs
156
              (B) TYPE: nucleic acid
157
              (C) STRANDEDNESS: double
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(ii) MOLECULE TYPE: DNA (genomic)  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  166 ATGGCATGC TROCCCTCTT TEAGCCCAAA GCCGCTGC TCCTGGTGGA CGCACCAC  168 CRGGCTACC GCACCTTCTT TEACCCTCAAA GCCCTCTCC TCCTGGTGGA CGCACCACCAC  168 CRGGCGTCA CGCGGTTGGC CAAAAGCCTC CCACACCACCGTG  170 CAGGGGGTCA AGGGCTTGGC CAAAAGCCTC CTCAAGGGCC TAAAGGGAC CGGGAGCTG  180  171 CAGGGGCT AGGGCCCCCAC CCCGGAGGAC TTCTTCCGCC AGAGGCCTA CAAGGGCCT  181  172 GTGGTGGTGG TCTTTGAGGC CAAGGCCCCC ACGAGGCCTA CATCAAGGGA  173 AAGCGGGCC GGGCCCCCAC CCCGGAGGAC TTTTCCCCCGC AGAGGCCTA CATCAAGGGA  174 ATGCTGGCCC TCCTTAGGCCT TTTGCGCCTG GAGGTTCCCG GATTGAGGC GACACCCTG  175 TTGGTGGACC TCCTTAGGGCC TTTTGCGCCTG GAGGTTACCACCACCCCACC	158	(D) TOPOLOGY: 1:	inear							
166 ATGGCATGC TROCCCTCTT TGACCCCAAA GCCCGCGTC TCTGGTGGA CGGCACCAC 168 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GCCTACCA CCAGCGCGG GAACCCGTT 120 170 CAGGCGGTCT ACGGCTTCGC CAAAAGCCTC CTCAAGGCC TGAAGGAGGA CCGGGACCGTG 180 172 GTGGTGTGTG TCTTTGAGC CAAAGCCCTC CTCAAGGCC TGAAGGAGGA CCGGGACCGTG 240 174 AAGCGGGCC GGCCCCAC CCGGAGGAC TTTCCCCCGC ACGAGGCCTA CAAGGCCTAC 240 175 CTGGCGAGCC TGCTTGACCG GCGGAGAAG TTTCCCCCGC ACGAGGCCT CATCAAGGAG 300 176 TTGGTGGACC TCCTAGGCCT TGTGCGCTG GAGGGTTCC GCTTTGAGGC GAGCACCTG 480 178 CTGGCCACCC TGGCCAAGCC GCGGAAAGA GAGGGTTAC AGGTCGCAT CCTCAACGAC 480 180 GACCCCCCC TGCCCAAGCC CTTTTCCGAC CCCATCAGCCA TCCTCCACCC TGAGGGTAC 480 181 CTGATCACCC CGCCTGGCT TTACCAAGA TACATCCCCC GGCTCAAGG CATCGCGGAG 660 184 TACCGGCC TGCGGGGA CCCTTGCGAT ACATCCCCC GGGTCAAGG CATCGGGGA 600 186 AAGACCGCC AGAGGCTCAT CCGCGAGAG GTGCGGGAG GTGGGGGA 610 187 CTGCGAAGA ACCCTCCTT GCGGGAGAG CTCCCAGGGG GAAAACCTCTT CCAGCACCTG 660 188 GACCAGCTGA ACCCTCCTT GCGGGAGAG CTCCCAGGGG GAAAACCTCTT CCAGCACCTG 720 190 TCCCGGAAGC TTTCCAGGT GCACACTCAC CTCCCCCTGG AGGTGGACT CGGGAGGCCC 780 191 CTCCACGAAT TCCGCCTCCT GAGGGGCC CTCCCCCTTGC AGGTGGACCT TGGAAGCCT 720 194 CTCCACAGAT TCGGCCTCCT GAGGGGGCC CTCCCCCTTGCG AGGTGGACC CTTGCACCCCT 720 195 CCGGAAGGGC CTTTTTTGG CTTTTCCTTT TCCCTCCCC ACCCAGGCCC CTGCCCCCTT 720 196 CCGGAAGGGC CTTTTTTGG CTTTTCCTTT TCCCTCCCC ACCCAGGCCC CTGCCCCCTT 720 197 CCGGAAGGCC CTTGAGGGGC CTTCTTTCCTTT TCCCTCCCC ACCCAGGCCC CTTTTGGGCC 1020 198 CTGCCCTGC CTGGGGCGTG GAGGGGCC CTCCATCGG CACAAGACC CTTTGGGCC 1020 199 CTGCGAAGGC CTTAAGGGGT GCGGGGAAT CTGCCAAGACC CTTTGGGCC 1020 190 CTGCAGAGC CTTAAGGGGT GCGGGGAAT CTGCCAAGACC CTTTGGGCC 1020 190 CTGCAGAGCC CTGCCCCTG GGGGGAAT CTGCCAAGACC CTTTTGGGC 1020 190 CTGCAGAGCC CTGCCTCCT GCCCAAGGCC CTCCTCCAG CCCCCAAGACCC CTTCCTCGCC CACCCCT 1020 190 CTGCAGAGCC CTGCCCCCT GCCCAAGACC CTCCCCCTGA CCCCCAAGACCC CTCCTTAGGGC 1020 190 CTGCAGAGAC CTAACGGGC CTCCCTTTCCGGC CACCCCCT CCCCCCCCC CCCCCCCCCC	160	(ii) MOLECULE TYPE: DI	NA (gend	omic)						
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180 GACCGCGACC TCTACCAGCT CCTTTCGGAG CGCATCGCCA TCCTCCACC TGAGGGGTAC 480 182 CTGATCACCC CGGCGTGGCT TTACGAGAG TACGGCCTCC GCCCGGACCA GTGGGTGGAC 540 184 TACCGGGCCC TGGCGGGGGGA CCCCTCGGAT AACATCCCG GGGTGAAGGG CATCGGGGAG 600 186 AAGACCGCC AGAGGCTCAT CCGCGAGTGG GGGACCTG AAAACCTCT CCAGCACCTG 660 188 GACCAGGTGA AGCCCTCCTT GCGGGAGAAC CTCCAGGCGG GCATGGAGGC CTGGCCCTT 720 190 TCCCGGAAGC TTTCCCAGGT GCACACTGAC CTCCCCCCTG AGGTGGACT TGGGAGGCC 780 192 CGCACACCCA ACTGGAGGG TCTGCGGGCT TTTTTGGAC GGTTGGAGTT TGGAGAGCC CTGCCCCCT GAGGAGGCC ACCCCAGT TCGGCCTCT TCGCGCACCA AGGCGCCC 780 194 CTCCACCAGT TCGGCCTCCT GGAGGGCCC AAGGCGCCA GGACGCCCC TGGCCCCCT 900 195 CTGGACGCTG CTTTTTGGG CTTTTTCCTT TCCCGTCCA GACCCATCTG GGCCGAGTT 760 196 CCGGAAGGGC CTTAAGGGGT GCGGGAATC CTGCCCAGC AGCCCATCTT TTGCCCTCCA GCCCACTCT TTTGCCCCC ACCCATCT TCTGCCCACAC CCTTTAGGGC 1080 197 CTGAGGACC TTAAGGGGT GCGGGAATC CTGCCCAGC ACCCATCT TCTGGCCTA CTCTTTGCCCT 1180 198 CTGGCCTTG CTGACCTCTT CCCCAGAGAC ACCCCATCT TCTGGCCTA CTTTTGCCCTT 1180 199 CCCTCCAACA CCACCCTGA GGGGTGGCC CTCTTCCACCA GCGGGAGTC TCTTCGCCTA 1140 190 CCCTCCAACA CCACCCCTG GGCGGAATC CTCTTCCACC CCTTTCCACCA CCCTTAAG GCCCTTTAG 120 190 GCCGGGGAGA GGCCCTCCT GCCCGAGCCC CTTTCCACCA CCCTAACACAC CCCTTTAAG 120 191 GCCCGGATG AGCCACCTC GCTCGAGCC CTCTTCCACA CCCTAACACAC CCCGGTCTT GCTTAAGCA GAGGTGACA ACCCGTTTC CCGGGTTTC CCGGGTGACA ACCCGCTTC GCTTAAGC GAGGTGACA ACCCGTTTC CCGGGTTTC CTGACCACC CTCTTCCACA CCCTAACACAC ACCCCCCCC CTGCTCTGCC CGGCTCCT TAGCGACCC CTCTTCCACA CCCACCCC TAGCACACCC CCCACCCC TAGCACCC CCCACCCC TAGCACCC CCCACCCC TAGCACCCC CCCACCCC TAGCACCCC CCCACCCC TAGCACCC CCCACCCC CCCCCCC CCCCCCCCC CCGGCTCCC CCCCCCC CCCCCC CCCCCC CCCCCCC CCCCCC	176	TTGGTGGACC TCCTAGGCCT TGTC	CGGCTG	GAGGTTCCCG	GCTTTGAGGC	GGACGACGTG	360			
182 CTGATCACCC CGGCGTGGCT TTACGAGAAG TACGGCCTGC GCCCGGAGCA GTGGGTGGAC 184 TACCGGCCCC TGGCGGGGGA CCCCTGGGAT AACATCCCCG GGGTGAAGGG CATCGGGAG 186 AACACCGCCC AGAGGCTCAT CGCCGAGTGG GGGAGCCTGG AAAACCCTCTT CAGAGCCCTG 186 AACACCGCCC AGAGGCTCATT CGCGGGAGAG CTCCAGGCGG GCATGGAGGC CCTGGCCCTT 190 TCCCGGAAGG TTTTCCAGGT GCACACTGAC CTGCCCCTG AGGTGGAGCT CGGGAGGCC CTGCACCCA ACCTGGAGGG TCTGCGGGCT TTTTTGGAGC GGTTGGAGCT CGGGAGGCC CTGCACCCA ACCTGGAGGG TCTGCGGGCC TTTTTGAGAC GGTTGGAGCT CTGCAGCCCC ACCTGAGAGCC CTTGCAGCCCC AAGAGCCCC CTGGCCCCT 900 196 CCGCAACGGG CTTTTTTGGG CTTTTCCTTT TCCCTTCCG AGCCCACTGG GCCGAGCT 960 198 CTGGCCCTG CTGGGCCTCT GCAGGGGCC CTCCATCGG CACAAGACC CTTAAGGGGC CTCCATCGG CACAAGACC CTCAACGG CACAAGACC CTCAACGG CCCAAGGACC CTCAATCGG CACAAGACC CTTAAGGGGC CTCCATCGG CACACGAGC CTCAACGG CACACACACC CACCCCTG CGGGCAAC CACCCCATG GGGGGAAT CTGGCCCAACG ACCCCATAGG CACCCAACGAC CACCCCTTA CGGGCAACG CACCCCATGC GCGGGAGAC CCCTTAAGGG CCCTTAAGGGAC CTCTATCGAC CCCTCAACGA CCCCCCCTG GGCCGAGCGC CTCTTCACA CCCCCCAACG AGCCCCATCAC CCCCCCTG GGCCGAGCC CTCTTCACA CCCTCAACGA CGCCCTTAA GGGGGGAGA AGCCGAGGAG CGCCCTTAA GCCCGGAGAG CGCCCTTAA GCCCGGAGAG CGCCCTTAA GCCCGGAGAG CGCCCTTAA GCCCGGAGAG AGCCCACCCC CTCTTCACAC CCCTCAACGA GGCCCTTACG GACGTGGCC CCTCTAACGA GCCCCTTAA GCCCGGAGTG CACGTGGAG GGCCCTCAC CCCTCCACC ACCTCACCC CCCTCCACC CCCTCCACC ACCTCACCC CCCTCCACC ACCTCACCC CCCTCCACC CCCTCCCCC CACGTGGAGGCC CACCTGAGA GACCGAGGAT CCCTCACCA CCCTCCACC CCACCCCCCT ACCCCCCC CACGCCCCC ACCCCCCCC CCCCCCCCC CCCCCCCC	178	CTGGCCACCC TGGCCAAGCG GGCC	GAAAAG	GAGGGGTACG	AGGTGCGCAT	CCTCACTGCC	420			
184 TACCGGGCCC TGGCGGGGGA CCCCTCGGAT AACATCCCCG GGGTGAAGGG CATCGGGGAG 660 186 AAGACCGCCC AGAGGCTCAT CCGCGAGTGG GGGAGCCTGG AAAACCTCTT CCACACCTG 660 188 GACCAGGTGA AGCCCTCCTT GCGGGAGAGA CCTCCAGGCGG GCATGGAGGC CTGGCCCTT 720 190 TCCCGGAAGC TTTCCCAGGT GCACACTGAC CTGCCCCTG AGGTGAGGCT CGGGAGGCCC 780 192 CGCACACCCA ACCTGGAGGG TCTGCGGGCT TTTTTGGACC GGTTGGAGCT TGGAGGGCC 780 194 CTCCACGAGT TCGGCCTCCT GGAGGGGCCC AGGCGGCAG AGGAGCCCC CTGGCCCCTT 900 195 CCGGAAGGGG CTTTTTTGG CTTTTCCTTT TCCCGTCCCG	180	GACCGCGACC TCTACCAGCT CCT	TCGGAG	CGCATCGCCA	TCCTCCACCC	TGAGGGGTAC	480			
186 AAGACCGCCC AGAGGCTCAT CCGCGAGTGG GGGAGCCTGG AAAACCTCTT CCAGCACCTG 188 GACCAGGTGA AGCCCTCTT GCGGAGAGA CTCCAGGCG GCATGGAGGC CCTGGCCCTT 720 190 TCCCGGAAGC TTTCCCAGGT GCACACTGAC CTGCCCCTG AGGTGGAGT CGGGAGGGC CTGCGCCTT 720 191 CCCGGAAGCC ACCTGAGGG TCTGCGGGCT TTTTTTGGAG GGTTGGAGTT TGGAGCCCC AGCTGAACCCA ACCTGAGGG TCTGCGGGCT TTTTTTTTTGAGC GGTTGGAGTT TGGAGCCCC 780 192 CGCACACCCA ACCTGAGGG TCTGCGGGCT TTTTTTTTTT	182	CTGATCACCC CGGCGTGGCT TTAC	CGAGAAG	TACGGCCTGC	GCCCGGAGCA	GTGGGTGGAC	540			
188 GACCAGGTGA AGCCCTCCTT GCGGGAGAAG CTCCAGGCGG GCATGGAGGC CTGGCCCTT TCCCGGAGCC TTTCCCAGGT GCACACTGAC CTGCCCCTGG AGGTGGAGTT CGGGAGCGC 780 192 CGCACACCCA ACCTGGAGGG TCTGCGGGCT TTTTTGGAG GGTTGGAGTT TGGAAGCCTC 640 194 CTCCACGAGT TCGGCCTCCT GGAGGGCCC AAGGGGCCC AGGAGCCCC CTGGCCCCCT 900 195 CCGGAAGGGG CTTTTTTGGG CTTTTCCTTT TCCCGTCCC AGCCCATGTG GGCCGACCTT 960 198 CTGGCCCTGG CTGGGGCTG GGAGGGCCC CTCCATCGGG CACAAGACCC CCTAGGGGC 1020 199 CTGAGGGACC TTAAAGGGGT GGGGGGAACCT CCCACAGGAGCCC CTTCAGGGC 1020 190 CTGAGGGACC TTAAAGGGGT GGGGGGAACCT CCCGCCAGG ACCTGGCGCGT TTTGGCCCTG 1080 190 CTGAGGGACC TGAAGGAGC CCCACAGGAGACC CCTTAGGGC 1020 190 CTGAGGGACC TTAAAGGAG GGGGGAACCT CCCGGCAAGA ACCTGGCGCGT TTTGGCCCTG 1080 190 CGCGGGAGGC CACACACAC CCACCCCTA GGGGGGAACCT CCCGCAAGGA ACCTGGCGCGT TTTGGCCCTG 1080 190 CCCGCAACA CCACCCCTA GGCGCAGCC CTCTTCCAG CCCTAAAGGA GCGCCTTAAG 1200 190 GCGGGGAGA GGCCCTCCT GCCCGAGCCC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG 1200 190 GCCCGGATGG AGGCCACGG GGTCCGGCC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG 1200 191 GCCCGGATGG AGGCCACGG GGTCCGGCC CACCTGGAG AGCCGCTTTC CCGGGTTTC 1320 191 GCCCGGATGG AGGCCACGG GGTCCGGCC GAGGGGCT ACCTCACGC CGGCCACCC 1440 192 GAGAACACCA ACCCCCAC CCGCCGAGCGC CACCTGGAG CACCGCACCC 1440 192 GAGAACACCT ACCACCCAC CCGCCACCCA TCCCCACCA GCGCCCTCC GGGCCTCCC 1440 193 CTCCCCGCA ACCCCAC CCCCCCC CTGCCCC CTGCCCCC CTGGCCCC CCACCCCC 1440 194 CCCCCCCACA CACCCCAC CCCCCCC CTGCCCC CTGCCCCC CCAAGCCG CCGCCCCCC 1440 195 CCCCACCCA ACCACACCGC CCCCCCCC CTGCCCC CTGGCCCC CCAAGCCG CCGCCCCCC 1440 195 CCCCACCCA ACCACACCGC CCCCCCCC CTGCCCCC CTGGCCCC CCAAGCCG CCGCCCCCC CTGCCCCC CTGCCCCC CTGCCCCC CTGCCCCC CTGGCCCC CCAAGCCG CCGCCCCCC CTGCCCCC CTGCCCCC CTGGCCCC CCAAGCCCC CCCCACCCCC CTGCCCCC CTGGCCCC CCACCCCCC CTGCCCCC CCAAGCCG CCGCCCCCC CTGCCCCC CTGGCCCC CCACCCCCC CCCCACCCCC CCCCCCCCCC	184	TACCGGGCCC TGGCGGGGGA CCCC	CTCGGAT	AACATCCCCG	GGGTGAAGGG	CATCGGGGAG	600			
190 TCCCGGAAGC TTTCCCAGGT GCACACTGAC CTGCCCTGG AGGTGGACTT CGGGAGGCCC 780 192 CGCACACCCA ACCTGGAGGG TCTGCGGGCT TTTTTGAGAC GGTTGAGAGTT TGGAAGCCTC 840 194 CTCCACGAGT TCGGCCTCCT GGAGGGCCG AAGGCGCCC GTGGCCCCCT 900 195 CCGGAAGGGC CTTTTTTGGG CTTTTTCTTT TCCCGTCCCG	186	AAGACCGCCC AGAGGCTCAT CCGC	CGAGTGG	GGGAGCCTGG	AAAACCTCTT	CCAGCACCTG	660			
192 CGCACACCCA ACCTGGAGGG TCTGCGGGCT TTTTTGGAGC GGTTGGAGTT TGGAAGCCTC 7900 194 CTCCACGAGT TCGGCCTCCT GGAGGGGCCG AAGGCGCAAGGCCCC CTGGCCCCCT 900 195 CCGGAAGGGG CTTTTTTGGG CTTTTCCTTT TCCCGTCCCG	188	GACCAGGTGA AGCCCTCCTT GCGC	GAGAAG	CTCCAGGCGG	GCATGGAGGC	CCTGGCCCTT	720			
194 CTCCACGAGT TCGGCCTCCT GGAGGGCCC AAGGCGCAG AGGAGGCCCC CTGGCCCCCT 196 CCGGAAGGGG CTTTTTTGGG CTTTTTCCTTT TCCCGTCCCG	190	TCCCGGAAGC TTTCCCAGGT GCAC	CACTGAC	CTGCCCCTGG	AGGTGGACTT	CGGGAGGCGC	780			
196 CCGGAAGGGG CTTTTTTGGG CTTTTCCTTT TCCCGTCCCG	192	CGCACACCCA ACCTGGAGGG TCTC	CGGGCT	TTTTTGGAGC	GGTTGGAGTT	TGGAAGCCTC	840			
198 CTGGCCTGG CTGGGGCGTG GGAGGGGCGC CTCCATCGGG CACAAGACCC CCTTAGGGGC 1020 200 CTGAGGGACC TTAAGGGGT GCGGGAATC CTGGCCAAGG ACCTGGCGGT TTTGGCCCTG 1080 202 CGGGAGGGCC TGGACCTCTT CCCAGAGGAC GACCCCATGC TCCTGGCCCTA CCTTCTGGAC 1140 204 CCCTCCAACA CCACCCTGA GGGGGTGGCC CGGCGTTACG GGGGGGAGTG GACGGAGGAT 1200 205 GCGGGGGAGA GGGCCCTCT GGCCGACGCC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG 1260 208 GGAGAAGAAC GCCTGCTTG GCTTACGAG GAGGTGGAGA AGCCGCTTC CCGGGTTTC 1320 210 GCCCGGATGG AGGCACCGCG GTTCAGAGA GAGGTGGAGA AGCCGCTTC CCGGGTTTC 1320 211 GCCCGGATGG AGGCACCGG GGTCCGGCTG GACGTGGAG CCGCCTTGCTGA CCTCCTGGAC CCTCCTCTG 1380 212 GAGGTGGAG CGGAGGTGC CCAGCTGGAG GAGGAGGTT TCCCCCTGGC CGGCCACCC 1440 214 TTCAACCTCA ACTCCCGCGA CCAGCTGGAG GAGGAGGTCT TCCGCCTGC CGGCCACCC 1440 215 GCCATCGCA AGACGGAAA GACGGGAAA GACGGGTCT TTGACCAGGC GGCCACCC 1500 216 CCCACCCA AGACGGA CCAGCTGGAG CGGTGCTCT TTGACCAGGC GGCCACCC 1500 217 CTCGGAGAG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGAGGTC GGCCCTCCT 1500 218 CTGCGAGAG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGAGGTC CCCAGACCTC 1620 220 AAGAACACCT ACATAGACCC CTGGCCCGC CTGGTCCAC CCAAGCCTC GCGGCTCAC 1660 221 ACCAGCTTCA ACATAGACCC CTGGCCCAC CCGGAGCCTT CAGCTCCGA CCCCAACCCTG 1740 222 ACCGCTTCA ACAAGACCC CCTCTGGGC GGCAGCCTT CAGCTCCGA CCCAACCCTG 1740 224 CAGAACATC CCGTGCCAC CCCTCTGGGC GCAGGCTTT CCAGCTCCGA CCCAACCCTG 1740 225 CAGAGACCA TCACATTCGG GTTTCCCC GAAGGGTTA GACCTCGGT CCTGGCCAC 1860 226 CTCTCCGGGA ACCTT GATCCGGGT TTTCAGCAGG GAGGGACAT CCACACCCAG 1920 230 ACCGCCACC TGATGTCG CGTTTCCCC GAAGGGGTAG ACCCTTCTAT GCGCCGAG 1920 231 ACCGCCACC TCAACATTCG GGTGCTCTAC GAGGGGTAG ACCCTCTGAT GCGCCGCG CGCACCCC CTACGCACCC CTACGAGCCA CCACACCCAG 1920 232 GCCAAGACCA TCAACTTCGG GGTGCTCTC GAGGGGGG GAGGGACAT CCACCCCAG 1920 233 ACCGCCACC TCACACG CCTTCACC GAAGGGGTAG ACCCTCTGAT CCACCCCC CACAGCCCC CCACACCCCC CCACACCCC CCACACCCCC	194	CTCCACGAGT TCGGCCTCCT GGAC	GGGCCG	AAGGCGGCAG	AGGAGGCCCC	CTGGCCCCCT	900			
198 CTGGCCTGG CTGGGGCGTG GGAGGGGCGC CTCCATCGGG CACAAGACCC CCTTAGGGGC 1020 200 CTGAGGGACC TTAAGGGGT GCGGGAATC CTGGCCAAGG ACCTGGCGGT TTTGGCCCTG 1080 202 CGGGAGGGCC TGGACCTCTT CCCAGAGGAC GACCCCATGC TCCTGGCCCTA CCTTCTGGAC 1140 204 CCCTCCAACA CCACCCTGA GGGGGTGGCC CGGCGTTACG GGGGGGAGTG GACGGAGGAT 1200 205 GCGGGGGAGA GGGCCCTCT GGCCGACGCC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG 1260 208 GGAGAAGAAC GCCTGCTTG GCTTACGAG GAGGTGGAGA AGCCGCTTC CCGGGTTTC 1320 210 GCCCGGATGG AGGCACCGCG GTTCAGAGA GAGGTGGAGA AGCCGCTTC CCGGGTTTC 1320 211 GCCCGGATGG AGGCACCGG GGTCCGGCTG GACGTGGAG CCGCCTTGCTGA CCTCCTGGAC CCTCCTCTG 1380 212 GAGGTGGAG CGGAGGTGC CCAGCTGGAG GAGGAGGTT TCCCCCTGGC CGGCCACCC 1440 214 TTCAACCTCA ACTCCCGCGA CCAGCTGGAG GAGGAGGTCT TCCGCCTGC CGGCCACCC 1440 215 GCCATCGCA AGACGGAAA GACGGGAAA GACGGGTCT TTGACCAGGC GGCCACCC 1500 216 CCCACCCA AGACGGA CCAGCTGGAG CGGTGCTCT TTGACCAGGC GGCCACCC 1500 217 CTCGGAGAG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGAGGTC GGCCCTCCT 1500 218 CTGCGAGAG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGAGGTC CCCAGACCTC 1620 220 AAGAACACCT ACATAGACCC CTGGCCCGC CTGGTCCAC CCAAGCCTC GCGGCTCAC 1660 221 ACCAGCTTCA ACATAGACCC CTGGCCCAC CCGGAGCCTT CAGCTCCGA CCCCAACCCTG 1740 222 ACCGCTTCA ACAAGACCC CCTCTGGGC GGCAGCCTT CAGCTCCGA CCCAACCCTG 1740 224 CAGAACATC CCGTGCCAC CCCTCTGGGC GCAGGCTTT CCAGCTCCGA CCCAACCCTG 1740 225 CAGAGACCA TCACATTCGG GTTTCCCC GAAGGGTTA GACCTCGGT CCTGGCCAC 1860 226 CTCTCCGGGA ACCTT GATCCGGGT TTTCAGCAGG GAGGGACAT CCACACCCAG 1920 230 ACCGCCACC TGATGTCG CGTTTCCCC GAAGGGGTAG ACCCTTCTAT GCGCCGAG 1920 231 ACCGCCACC TCAACATTCG GGTGCTCTAC GAGGGGTAG ACCCTCTGAT GCGCCGCG CGCACCCC CTACGCACCC CTACGAGCCA CCACACCCAG 1920 232 GCCAAGACCA TCAACTTCGG GGTGCTCTC GAGGGGGG GAGGGACAT CCACCCCAG 1920 233 ACCGCCACC TCACACG CCTTCACC GAAGGGGTAG ACCCTCTGAT CCACCCCC CACAGCCCC CCACACCCCC CCACACCCC CCACACCCCC	196	CCGGAAGGG CTTTTTTGGG CTTT	TCCTTT	TCCCGTCCCG	AGCCCATGTG	GGCCGAGCTT	960			
200         CTGAGGGACC         TTAAGGGGGT         GCGGGGAATC         CTGGCCAAGG         ACCTGGCGGT         TTTGGCCCTG         1080           202         CGGGAGGGCC         TGGACCTTT         CCCAGAGGAC         GACCCCATGC         TCCTGGCCTA         CCTTCTAGAC         1140           204         CCCTCCACAC         CCACCCTGA         GGGGGGCC         CCGCGTTACG         GGGGGGAGT         1200           206         GCGGGGGAG         GGCCCTCCT         GGCCGAGGC         CTTTTCCAGA         CCCTAAAGGA         GGCCTTAG         1260           208         GGAGAAGAAC         GCCTGCTTT         GCTTTACGAG         GAGGTGGAG         CCGCGCATC         1320           210         GCCCGGATG         AGCCCACGG         GGCTGGGG         CCAGCTGGAG         CAGGTGGAG         CCGCCACCC         1440           212         AGAGTGGAG         AGCCGCAGG         CCAGCTGAG         CAGGGGAGA         AGCGGCAGG         CCAGCTGCC         1500           216         GCCATCGCA         ACACCGCAGA         GACGGGAAA         GACGGGAAA         CCCTCACCCA         GCGCTGCCT         CCTGGAGGC         1500           216         CCCGCTCCA         ACCAGCCACC         CCTGCCCACC         CCGGTGCCGC         CCGGCCCCCC         1620           221         AACAACATC	198	CTGGCCCTGG CTGGGGCGTG GGAC	GGGCGC	CTCCATCGGG	CACAAGACCC	CCTTAGGGGC	1020			
202 CGGGAGGGCC TGGACCTCTT CCCAGAGGAC GACCCCATGC TCCTGGCCTA CCTTCTGGAC 204 CCCTCCAACA CCACCCTGA GGGGGTGGCC CGGCGTTACG GGGGGAGTG GACGAGGAT 1200 205 GCGGGGAGA GGGCCCTCCT GGCCGACGCC CTCTTCCAGAC CCCTAAAGGA GCGCCTTAAG 208 GGAGAAGAC GCCTGCTTTG GCCTTACAGA GAGGTGGAGA AGCCGCTTTC CCGGGTGTTG 208 GGAGAGAC GCCTGCTTTG GCTTTACAGA GAGGTGGAGA AGCCGCTTC CCGGGTGTTG 209 GCCCGGATGG AGGCCACGGG GGTCCGCCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG 200 GCCCGGATGG AGGCCACGGG GGTCCGCCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG 201 GCCCGGATGA GAGCCACGCG GACGTGGAG CGGGTGCTT TCCGCCTGC CGGCCTCCCC 1440 214 TTCAACCTCA ACTCCGCGA CCACCTGAGA CGGCTGCCT TTCACGAGCT GGCCTGCCT 1500 216 GCCATCGGCA AGACGGAAAA GACGGGGAAA CGCTCCACCA GCGCTGCCT GCTGGAGGCC 1560 217 CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTCCACCA GCGCTGCCT GCTGGAGGCC 1560 218 CTGCGAGAGG CCCACCCCAT CGTGGCCCGC CTGGTCCACC CCAAGACCGC CCGGCTCCAC 1660 219 AAGAACACCT ACATAGACCC CCTGCCCGC CTGGTCCACC CCAAGACCGC CCGGCTCCAC 1660 220 AAGAACACCT ACATAGACCC CCTGCCCGC CTGGTCCACC CCAAGACCGC CCGGCTCCAC 1660 221 ACCCGCTTCA ACCAGACGC CACCCCCAG GGCAGCCTT CACCAAGCCG CCGGCTCCAC 1660 222 ACCCGCTTCA ACCAGACGC CACCCCAG GGCAGCCTT CACCAACCTG 1740 224 CAGAACATCC CCGTGGGCA CCCTCTGGGC CAGCGCATC GCCGAGCCTT CGTGGCCGAG 1800 225 GAGGGCTGG TGCTGTGGT CTTGGACTAC AGCAGACTC CCCAACCCAG 1800 226 CTCTCCGGG ACGAGACCT GATCCGGGT TTTCAGGAG GGAGGGACAT CCACACCAG 1920 230 ACCGCCAGCT GGATATTCGG CGTTTCCCCC GAAGGGGTAA ACCCTCTGAT GCGCCGGGCG 1980 231 ACCGCCAGCT GGATCTTCGG CGTTTCCCCC GAAGAGGTAA ACCCTCTGAT GCGCCGGGCG 1980 232 GCCAAGACCA TCAACTTCGG GGTGCC TTCATTGAC GCCCACCCCC CTCCGGGGC 2040 234 CTTTCCATCC CCTACGAGA GGCGGTGGC TTCATTGAC CCCCACCGCCT CTCCGGGGAG 2040 235 AACGTGCGG CTTGATTGG CGTTTTCCCCG GAAGGGCTA CCCCACCCC CCACCCCC CCACCCCC CCACCCCC CCACCCCC CCCACGCCC CCACCCCC CCACCCCC CCACCCCC CCACCCCC CCACCCCC CCACCCCC CCCCCC							1080			
206 GCGGGGGGAGA GGGCCCTCCT GGCCGAGCGC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG 208 GGAGAAGAAC GCCTGCTTTG GCTTTACGAG GAGGTGGACA AGCCGCTTTC CCGGGTGTTG 1320 210 GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCT ACCTCCAGGC CCTCTCCCTG 1380 212 GAGGTGGAG CGGAGGTGCC CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCCC 1440 214 TTCAAACCTCA ACTCCCGCGA CCAGCTGGAG CGGGTGCTC TTGACCAGGC GGCCACCCC 1500 216 GCCATCGGCA AGACGGAGAA GACGGGAAA CGCTCACCA GCGCTCCCGT GCTGAGGGC 1560 218 CTGCGAGAGG CCCACCCCAT CGTGGACGC ATCCTGCAGT ACCGGGAGGTC CACCAAGCTC 1620 220 AAGAACACCT ACATAGACCC CCTGCCCGC CTGGTCCACCA GCGCTCCCAC CCGGCTCCAC 1680 222 ACCCGCTTCA ACCAGACGGC CACCGCCAC GGCAGCTT CCACAAGCTC 1620 224 CAGAACATCC CCGTGCGCA CCCTCTGGC CACCGCACCC CCCAACCCTG 1740 224 CAGAACATCC CCGTGCGCAC CCCTCTGGC CACCGAGCTT CCAGCCCCAC CCCCAACCTG 1740 224 CAGAACATCC CCGTGCGCAC CCCTCTGGC CACCGAGTT ACCTTCGAG CCCCAACCTG 1740 225 CTCTCCGGGG ACGAGAACCT GATCCGGGT CTTTCAGGAGG GGAGGCTT CGTGGCCCAC 1860 228 CTCTCCGGGG ACGAGAACCT GATCCGGGT CTTTCAGGAGG GGAGGGACAT CCACACCCAG 1920 230 ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGCGC 1980 232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATCCC CCCACCCCAC	202	CGGGAGGGCC TGGACCTCTT CCCA	GAGGAC	GACCCCATGC	TCCTGGCCTA	CCTTCTGGAC	1140			
206 GCGGGGGGAGA GGGCCCTCCT GGCCGAGCGC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG 208 GGAGAAGAAC GCCTGCTTTG GCTTTACGAG GAGGTGGACA AGCCGCTTTC CCGGGTGTTG 1320 210 GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCT ACCTCCAGGC CCTCTCCCTG 1380 212 GAGGTGGAG CGGAGGTGCC CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCCC 1440 214 TTCAAACCTCA ACTCCCGCGA CCAGCTGGAG CGGGTGCTC TTGACCAGGC GGCCACCCC 1500 216 GCCATCGGCA AGACGGAGAA GACGGGAAA CGCTCACCA GCGCTCCCGT GCTGAGGGC 1560 218 CTGCGAGAGG CCCACCCCAT CGTGGACGC ATCCTGCAGT ACCGGGAGGTC CACCAAGCTC 1620 220 AAGAACACCT ACATAGACCC CCTGCCCGC CTGGTCCACCA GCGCTCCCAC CCGGCTCCAC 1680 222 ACCCGCTTCA ACCAGACGGC CACCGCCAC GGCAGCTT CCACAAGCTC 1620 224 CAGAACATCC CCGTGCGCA CCCTCTGGC CACCGCACCC CCCAACCCTG 1740 224 CAGAACATCC CCGTGCGCAC CCCTCTGGC CACCGAGCTT CCAGCCCCAC CCCCAACCTG 1740 224 CAGAACATCC CCGTGCGCAC CCCTCTGGC CACCGAGTT ACCTTCGAG CCCCAACCTG 1740 225 CTCTCCGGGG ACGAGAACCT GATCCGGGT CTTTCAGGAGG GGAGGCTT CGTGGCCCAC 1860 228 CTCTCCGGGG ACGAGAACCT GATCCGGGT CTTTCAGGAGG GGAGGGACAT CCACACCCAG 1920 230 ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGCGC 1980 232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATCCC CCCACCCCAC	204	CCCTCCAACA CCACCCCTGA GGGC	GTGGCC	CGGCGTTACG	GGGGGGAGTG	GACGGAGGAT	1200			
208 GGAGAAGAAC GCCTGCTTTG GCTTTACGAG GAGGTGGAGA AGCCGCTTTC CCGGGTGTTG 210 GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG 212 GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCCC 1440 214 TTCAACCTCA ACTCCCGCGA CCAGCTGGAG CGGGTGCTC TTGACGAGCT GGGCCTGCCT 1500 216 GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC 1560 218 CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGGAGCT CACCAAGCTC 1620 220 AAGAACACCT ACATAGACCC CCTGCCCGCC CTGGTCCCC CCGAGGACCT CCGGCTCCAC 1680 222 ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGCCTT CCAGAGCCG CCGGCTCCAC 1680 224 CAGAACATCC CCGTGGCGC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCAC 1740 225 GAGGGCTGGG TGCTGGTGT CTTGGACTAC AGCCAGACTC CCCCAACCTG 1740 226 GAGGGCTGG TGCTGGTGT CTTGGACTAC AGCCAGATCT GTGGCCCAC 1860 227 CTCTCCGGG ACGACAACCT GATCCGGGT CTTCAGGAGG GGAGGACAT CCACACCCAG 1920 230 ACCGCCAGCT GGATGTTCCG CGTTTCCCC GAAGGGGTA ACCTCTGGT CCTGGCCCAC 1860 231 ACCGCCAGCT GGATGTTCGG CGTTTCCCC GAAGGGGTAA ACCTCTGAT GCGCCGGGCG 1980 232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGCCC CCCACCCCC CTCCGGGGG 1980 233 ACCCCCAGCT CCACCGAGA GGGGTGCC TTCATTGAGC CCCACCCCC CTCCCGGGGG 1980 234 CTTTCCATC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCCCCGCCT CTCCCGGGGG 1980 235 AAGGTGCGG CCTGGATTGA GGGGGGTGCC TTCATTGAGC GCCCCGCCT CTCCCGGGGG 2040 236 AAGGTGCGGG CCTGGATTGA GGGGGGGCC TTCATTGAGC GCCCGCGCG GTATGTGGAG 2100 237 ACCGCCAGCT CCCTCAGGAGA GGCGGTGGC CTCACCGCCC CCCCCCCCC CCCACCGCC CCCCCCCC 2100 238 ACCCTCTTCG GCCCGCGC CTTCAACATG CCGGGTGAA GAGCGTGCCC 2100 238 ACCCTCTTCG GCCCGGGC CTTCAACATG CCGGGCGG GATACTTCC CCTACGGGAG ACCGCCC CGACCTCATG 2220 240 GAGGCGCGG AGCGCATGGC CTTCAACATG CCGGGCGAGA GAGCGTCCC 2220 240 GAGGCGCGA AGCGCATGGC CTCCAAGGAC CGGCGCG CGACCTCATG 2280 241 CAGGTGCCA TGGTCCGCC CCCAAGGAC CGGCGCG GACCTCATG 2240 242 AAGCTGGCA ACGACTGGC CTCCAGAGAC CGGGGGAGA GATGCTTTTG 2240 244 CAGGGGGGAG AGGACTGGC CTCCAAGGAC CGGGGGAGA GATGCTTTTG 2240 245 TTGCCAAGG AGGCATGGC CTCCAGAGAC CGGCGC GGGGGAGA GATGCTTTTG 2240 246 TTGGCCAAGG AGGCTGGC CTCCCGCAAGGAC CCCCCACGGG GGGGGGGGGG							1260			
210 GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG 212 GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCCC 214 TTCAACCTCA ACTCCCGCGA CCAGCTGGAG CGGTGCTCT TTGACGAGCT GGGCCTGCCT 216 GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC 218 CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGGAGGCT CACCAAGCTC 210 AAGAACACCT ACATAGACCC CTGGCCCGC CTGGTCCACC CCAAGACCGC CCGGCTCCAC 220 AAGAACACCT ACATAGACCC CTGCCCACC GCGAGGCTT CACCAAGCTC 221 ACCCGCTTCA ACCAGACGGC CACCGCACC GGCAGGCTTT CCAGCTCCGA CCCCAACCTG 222 ACCCGCTTCA ACCAGACGC CACCGCACC GGCAGGCTTT CCAGCTCCGA CCCCAACCTG 224 CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCAC 225 GAGGGCTGGG TGCTGGTGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CTGGCCCAC 226 GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CTGGCCCAC 227 ACCGCCAGC TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CTGGCCCAC 228 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GAGGGACAT CCACACCAG 1920 230 ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG 1980 231 CTTTCCATCC CCTACGAGGA GGCGTGTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG 2040 232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG 2040 233 ACCCTCTTCG GCCGCGCG CTATGTGCC GAGCAGGGCC GCCGCGCGC CTACTGCCC 2100 234 AAGGTGCGGG CCTGGATTGA GGGGACCCT GAGGAGGGC GCCGCGCGC GACCTCACC 236 AAGGTGCGGG CCTGGATTGA GGGGACCCT GAGGAGGGC GCCGGCGGG GTATGTGGAG 2160 237 ACCCTCTTCG GCCGCGCGC CTATGTGCCC GACCTCACG CCCGGCGCG CTACTCCC CCACGGCGC CGACCTCATG 2220 240 GAGGCGGGG AGCGCATGC CTTCAACATG CCGGTCCAGG GACCTCCA GAGCTACCC 240 GAGGCGGCG AGCGCATGCC CTTCAACAG CCCGGGGG GTATGTGGAG 2240 241 CAGGTGCAC TGGTGCC CTTCAACAG CCCGGGGG GATGCTTTTG 2340 242 AAGCTGCAC AGGACTGGC CTTCAACAG CCCGGGGG GATGCCTTTTG 2340 244 CAGGTGCAC AGGACTGGC CTTCAACAG CCCGGGGG GATGCCTTTTG 2340 245 TTGGCCAAGG AGGACTGGC CTTCAACAG CCCCTGCAG GGGGGAG GATGCCTTTTG 2340 246 CTGGGGGA AGGACTGGC CTTCAACAG GCCCCCGC GGCGGAGA GGTAGCCGC 240 TTGGCCAAGG AGGACTGGC CTTCAACAG GCCCCCGCG GGGGGAG GTAGCCGT 2400 246 TTGGCCAAGG AGGACTGGC CTCCGCCAAG GAGTAG CCCCCTGCAG GGGGGAG										
212 GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCCC 1440 214 TTCAACCTCA ACTCCCGCGA CCAGCTGGAG CGGGTGCTCT TTGACGAGCT GGGCCTGCCT 1500 216 GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC 1560 218 CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGGAGCT CACCAAGCTC 1620 220 AAGAACACCT ACATAGACCC CCTGCCCGC CTGGTCCACC CCAAGACCGG CCGGCTCCAC 1680 221 ACCCGCTTCA ACCAGACGGC CACCGCCAC GGCAGGCTTT CAGGTCCCGA CCCCAACCTG 1740 222 CAGGACATCC CCGTGCGCCAC CCCTCTGGGC CAGCGATCC GCCGAGCCTT CGTGGCCGAG 1800 223 GCGAGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC 1800 224 CTCTCCGGGG ACGAGAACCT GATCCGGGT TTTCAGGAGG GGAGGGACAT CCACACCCAG 1920 230 ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT CCACACCCAG 1920 231 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG 1920 232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG 2040 233 CCTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC 2100 234 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCCCGCGGGG GTATGTGGAG 2040 235 AAGGTGCGGG CTTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGG GTATGTGGAG 2160 236 AAGGTGCGGG CTTGGATTGA GGGGACCCTC GAGCGCGCG CGACCTCCAC 2200 240 GAGGCGGGG AGCGCATGGC CTTCAACATG CCCGGGTGAA GAGCGTGCGC 2220 240 GAGGCGGCG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCCCCC CGACCTCATG 2280 242 AAGCTGGCCA TGGTGCGGCT TTTCCCCCG GTCCAGGACC GCGGCGGGG GATGCTCTTTTG 2340 244 CAGGTGCACA ACGACCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 2400 245 CTGGCCAAGG AGGCCTGGG CTTCAACATG CCCGAGGACC GGCGGGAGAG GGTAGCCGCT 2400 246 CTGGCCAAGG AGGCCTGGC CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 2400 246 CTGGCCAAGG AGGCCTGGG CTTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTGGGGGT 2400 247 CAGGTGCAAG AGGCCTGGC CCTCGAGGC CCCAAGGACC GGGCGGAGAG GGTGGAGGTG 2400 248 GGCCTGGGGG AGGACTGGC CCTCGAAGGCC CCCAAGGACC GGGCGGAGAG GGTGGAGGTG 2400 248 GGCCTGGGGG AGGACTGGC CTCCGAGGC CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG 2400 249 CTCTCAACATG AGGCCCTCAAGGCC CCCAAGGACC GGGCGGAGAG GGTGGAGGTG 2400 240 CTCTCAACAC ACGACCTGC CCCAAGGACC GGCGGGAGAG GGTGGCCT 2400 240							1380			
TTCAACCTCA ACTCCGCGA CCAGCTGGAG CGGGTGCTCT TTGACGAGCT GGGCCTGCCT  1500  216 GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC 1560  218 CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGAGAGCT CACCAAGCTC 1620  220 AAGAACACCT ACATAGACCC CCTGCCCGCC CTGGTCCACC CCAAGACCGG CCGGCTCCAC 1680  221 ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTT CCAGGTCCGA CCCCAACCTG 1740  222 CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG 1800  223 GAGGGCTGGG TGCTGGTGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC 1860  224 CAGAACATCC CGGTGCGAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCCAC 1860  225 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG 1920  230 ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGCGCG 1980  231 CCTACCACC CCTACAGAGA GGCGGTGGCC TTCATTGAGC CCCACCGCCT CTCCGGGGAG 2040  232 CCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG 2040  233 ACCCTCTTCG CCTGGAGGA GGGGACCCTC GAGGAGGGCC GCCGCCGCC CTCCGGGAG 2040  234 CTTTCCATCC CCTACGAGGA GGGGACCCTC GAGGAGGGCC GCCGCCGGG GTATGTGGAG 2160  235 AAGGTGCGGC CCTGGATTGA GGGGACCCTC GAGCACCCC GCCGCGCG GTATGTGGAG 2160  236 AAGGTGCGCG AGCGCATGGC CTTCAACAATG CCGGTCCAACG CCCGGGTGAA GAGCGTGCCC 2220  240 GAGGCGCGG AGCGCATGGC CTTCCACACAT CCGGTCCAACG CCCGGGCGG GATGTTTTG 2340  242 AAGCTGGCCA TGGTGCGCT TTTCCCCCGG CTTCAAGGAAC TGGGGGCGAG GATGCTTTTG 2340  244 CAGGTGCAC ACGAGCTGGT CCTCGAGGCC CCCACAGGACC GGGCGCAGAG GATGCTTTTG 2340  244 CAGGTGCAC ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGAGAG GATGCTTTTG 2340  245 TTGGCCAAGG AGGCTATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GATGCTTTTG 2340  246 TTGGCCAAGG AGGCTTGGT CCTCGAGGCC CCCACAGGACC GGGCGAGAG GATGCTTTTG 2340  247 AAGCTGGCAC ACGAGCTGGT CCTCGAGGCC CCCACAGGACC GGGCGAGAG GATGCTTTTG 2340  248 GCCTGGGGG AGGACTGGC CTTCCACAGG CCCCTGCAGG GGTGGAGGTG 2400  248 GCCTGGGGG AGGACTGGC CTCCCCCAAGGACC GGGCGAGAG GATGCTTTTG 2340  249 GCCTGGGGG AGGACTGGC CTCCCCCAAGGACC GGGCGAGAG GGTGGCGCT 2400  240 CTGCTCAACGAC AGGACTGGC CTCCCCCAAGGACC GGGCGAGAG GGTGCCCT 2400  241 CTCCCCTGAGG AGGCCTCTCAACG CCCCCCGCG CGCCCCCCCCCC										
216 GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC 1560 218 CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGGAGCT CACCAAGCTC 1620 220 AAGAACACCT ACATAGACCC CCTGCCCGCC CTGGTCCACC CCAAGACCGG CCGGCTCCAC 1680 222 ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCCAACCTG 1740 224 CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG 1800 226 GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC 1860 228 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG 1920 230 ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGCG 1980 232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG 2040 234 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC 2100 236 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGG GTATGTGGAG 2160 238 ACCCTCTTCG GCCGCCGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCTACCCC 2100 240 GAGGCGGGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCCCCC CGACCTCATC 2280 241 GAGCTGGCA TGGTGCGCC TTTCAACATG CCGGTCCAGG GCACCCCCC CGACCTCATG 2280 242 AAGCTGGCA AGGGCATGGC CTTCAACATG CCGGTCCAGG GCACCCCCC CGACCTCATG 2280 243 GCCAAGACA ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGCGGGAGAG GATGCTTTTG 2340 244 CAGGTGCAC ACGAGCTGGT CTCCCCCG CTCCAAGGACC GGCCGGAGAG GATGCTTTTG 2340 245 TTGGCCAAGG AGGACTGGT CCTCGAGGCC CCCAAGGACC GGCCGGAGAG GGTAGCCGCT 2400 246 TTGGCCAAGG AGGACTGGT CCTCCGCCAAG GAGTAG 247 CTTGGCCAAGG AGGACTGGT CCTCCGCCAAG GAGTAG 248 GGCCTGGGGG AGGACTGGT CTCCGCCAAG GAGTAG 249 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG 240 LTGGCCAAGG AGGACTGGCT CTCCGCCAAG GAGTAG 241 CTTCACCAGG AGGACTGGCT CTCCGCCAAG GAGTAG 242 LTGGCCAAGG AGGACTGGCT CTCCGCCAAG GAGTAG 243 CTTCACACCC CCAAGGACC GGCCGCC CGACCTCATG 2240 244 CAGGTGCAC ACGAGCTGGT CCTCCACAGG CCCCCCCACGCCGC CGACCTCATG 2240 245 LTGCCCTGGGG AGGACTGGCT CTCCGCCAAG GAGTAG 246 LTGCCCTGGAG AGGACTGGCT CTCCGCCAAG GAGTAG 247 CTCCCTGCAAG AGGACCTGCC CCCAAGGACC GGCGGAGAG GGTAGCCGCT 2400 247 CTCCCTGGAG AGGACTGGCT CTCCCCCGC CCCCACGCCGC GGCGGAGAG GGTAGCCTTCCCCGC CCCCCACGCCCC CAAGGACC GCCGCCGC GCGCGCGC										
218 CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGAGCT CACCAAGCTC 220 AAGAACACCT ACATAGACCC CCTGCCCGCC CTGGTCCACC CCAAGACCGG CCGGCTCCAC 221 ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCCAACCTG 222 ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCCAACCTG 223 CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCCAC 226 GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC 227 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG 230 ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG 231 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC 232 CCCAAGACCA TCAACTTCGG GGTGCTCTTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG 233 ACCCTCTTCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC 234 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCCGCGCGG GTATGTGGAG 235 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG 240 GAGGCGGCGG AGCGCTGGC CTATGTGCCC GACCTCAACG CCCGGCTGAA GAGCGTGCGC 240 GAGGCGGCGG AGCGCATGGC CTTCAACATG CCCGGTCCAGG GCACCCCGC CGACCTCATG 242 AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG 244 CAGGTGCACG ACGACTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 240 CAGGTGCACG ACGACTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 240 CAGGTGCACG ACGACTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 240 CAGGTGCAAGG AGGCTATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG 244 CAGGTGCACG ACGACTGGT CCTCCGCCAAG GCCCCCCGC GGACCTCATG 245 TTGGCCAAGG AGGACTGGT CTCCGCCAAG GAGTAG 246 TTGGCCAAGG AGGACTGGT CTCCGCCAAG GAGTAG 247 CACACCCCCTGCAAG GGTGGAGGTG CCCCTGCAGG TGCCCCTGGA GGTGAGCGCT 2400 248 GGCCTGGGG AGGACTGGC CTCCGCCAAGGACC GGCCGCGC GGACGCCGC 2400 241 CTTTCCATCC CCCCAAGGACC GGCCGCCGC CCCAAGGACC GGTGGAGGTG 246 TTGGCCCAAGG AGGACTGGCT CTCCGCCAAG GAGTAG 247 CTTTTTCCCCCGG CTCCAAGGAC GGTGGAGGGTG CCCCTGGAG GGTGAGCCGCT 2400 245 TTGGCCAAGG AGGACTGGC CTCCAAGGAC GGCGGAGAG GGTAGCCGCT 2400 246 TTGGCCAAGG AGGACTGGC CTCCAAGGAC GGCGCGCGC GGACGGCGC CCCAAGGAC GGCGCGC CCCAAGGAC GGTAGCCCCCCGC CCCAAGGAC GGTAGCCCCCCGC CCCAAGGAC GGCGCGCG										
220 AAGAACACCT ACATAGACCC CCTGCCCGCC CTGGTCCACC CCAAGACCGG CCGGCTCCAC 222 ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCCAACCTG 224 CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCCAC 226 GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC 228 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG 230 ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG 232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG 234 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACCTCCA GAGCTACCCC 236 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGG GTATGTGGAG 238 ACCCTCTTCG GCCGCCGGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGC 240 GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCCGCCG CGACCTCATG 242 AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG 244 CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGA GATGCTTTTG 244 CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGAGAG GGTAGCCGCT 246 TTGGCCAAGG AGGCTATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTAGCCGCT 246 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTAGCCGCT 246 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTAGCCGCT 246 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG 248 GGCCTGGGGG AGGACTGGT CTCCGCCAAG GAGTAG 2496 250 (2) INFORMATION FOR SEQ ID NO: 3: 252 (i) SEQUENCE CHARACTERISTICS:										
222 ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCCAACCTG 224 CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG 226 GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC 228 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG 230 ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG 232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG 234 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCC 236 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGG GTATGTGGAG 238 ACCCTCTTCG GCCGCCGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCCC 240 GAGGCGGCG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCG CGACCTCATG 242 AAGCTGGCCA TGGTGCGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG 244 CAGGTGCAC ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCCT 246 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCTGGA GGTGGCCC 240 GGCCGCGGG AGGACTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 240 CAGGTGCACG ACGACTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 240 CAGGTGCACG ACGACTGGT CCTCCGCCAAG GAGTAG 242 AAGCTGGCG AGGACTGGT CTCCCCCAAGGACC GGGCGGAGAG GGTAGCCGCT 2400 244 CAGGTGCACG ACGACTGGT CTCCCCCAAGGACC GGGCGGAGAG GGTAGCCGCT 2400 245 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG 2460 247 CAGGTGCACG AGGACTGGT CTCCCCCAAGGACC GGGCGGAGAG GGTAGCCGCT 2400 248 GGCCTGGGGG AGGACTGGCT CTCCCCCAAG GAGTAG 2496 250 (2) INFORMATION FOR SEQ ID NO: 3:										
224 CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG 226 GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC 228 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG 230 ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG 232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG 234 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC 236 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG 238 ACCCTCTTCG GCCGCCGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGC 240 GAGGCGGCG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCG CGACCTCATG 242 AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG 244 CAGGTGCAC ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGCGGAGAG GGTAGCCGCT 246 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCTGGA GGTGGAGGTG 248 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG 2496 250 (2) INFORMATION FOR SEQ ID NO: 3: 252 (i) SEQUENCE CHARACTERISTICS:										
226 GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC  228 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG  230 ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG  232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG  234 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC  236 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGG GTATGTGGAG  238 ACCCTCTTCG GCCGCCGGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGC  240 GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCCGCCG CGACCTCATG  241 CAGGTGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG  242 AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG  244 CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT  246 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG  248 GGCCTGGGG AGGACTGGT CCTCCGCCAAG GAGTAG  2496  250 (2) INFORMATION FOR SEQ ID NO: 3:  252 (i) SEQUENCE CHARACTERISTICS:										
228 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG 230 ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG 232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG 234 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC 236 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGG GTATGTGGAG 238 ACCCTCTTCG GCCGCCGGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGC 240 GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG 242 AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG 244 CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGA GGTAGCCGCT 246 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG 248 GGCCTGGGG AGGACTGGT CTCCGCCAAG GAGTAG 250 (2) INFORMATION FOR SEQ ID NO: 3: 252 (i) SEQUENCE CHARACTERISTICS:										
ACCGCCAGCT GGATGTTCGG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG  232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG  234 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC  236 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGG GTATGTGGAG  238 ACCCTCTTCG GCCGCCGGC CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGC  240 GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG  242 AAGCTGGCCA TGGTGCGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG  244 CAGGTGCAC ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGA GGTAGCCGCT  246 TTGGCCAAGG AGGTCATGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG  248 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG  250 (2) INFORMATION FOR SEQ ID NO: 3:  252 (i) SEQUENCE CHARACTERISTICS:										
232 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG 234 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC 236 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGG GTATGTGGAG 238 ACCCTCTTCG GCCGCCGGC CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGC 240 GAGGCGGCG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCG CGACCTCATG 242 AAGCTGGCCA TGGTGCGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG 244 CAGGTGCAC ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGA GGTAGCCGCT 246 TTGGCCAAGG AGGTCATGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG 248 GGCCTGGGGG AGGACTGGT CTCCGCCAAG GAGTAG 250 (2) INFORMATION FOR SEQ ID NO: 3: 252 (i) SEQUENCE CHARACTERISTICS:							_			
234 CTTTCCATCC CCTACGAGGA GGCGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC 2100 236 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG 2160 238 ACCCTCTTCG GCCGCCGGC CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGC 2220 240 GAGGCGGCG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCG CGACCTCATG 2280 242 AAGCTGGCCA TGGTGCGCT TTTCCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG 2340 244 CAGGTGCAC ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 2400 246 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG 2460 248 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG 250 (2) INFORMATION FOR SEQ ID NO: 3: 252 (i) SEQUENCE CHARACTERISTICS:						•				
236 AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGG GTATGTGGAG 238 ACCCTCTTCG GCCGCCGGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGC 240 GAGGCGGCG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG 242 AAGCTGGCCA TGGTGCGGCT TTTCCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG 244 CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 246 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG 248 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG 250 (2) INFORMATION FOR SEQ ID NO: 3: 252 (i) SEQUENCE CHARACTERISTICS:										
238 ACCCTCTTCG GCCGCCGGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGCGC 2220 240 GAGGCGGCG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG 2280 242 AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG 2340 244 CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 2400 246 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG 2460 248 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG 2496 250 (2) INFORMATION FOR SEQ ID NO: 3: 252 (i) SEQUENCE CHARACTERISTICS:										
240 GAGGCGGCG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG 242 AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG 2340 244 CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 246 TTGGCCAAGG AGGTCATGGA GGGGGTCTTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG 248 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG 2496 250 (2) INFORMATION FOR SEQ ID NO: 3: 252 (i) SEQUENCE CHARACTERISTICS:										
242 AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTTCAGGAAC TGGGGGCGAG GATGCTTTTG 2340 244 CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 246 TTGGCCAAGG AGGTCATGGA GGGGGTCTTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG 248 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG 250 (2) INFORMATION FOR SEQ ID NO: 3: 252 (i) SEQUENCE CHARACTERISTICS:							2280			
244 CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 246 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG 248 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG 250 (2) INFORMATION FOR SEQ ID NO: 3: 252 (i) SEQUENCE CHARACTERISTICS:			_							
246 TTGGCCAAGG AGGTCATGGA GGGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG 248 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG 250 (2) INFORMATION FOR SEQ ID NO: 3: 252 (i) SEQUENCE CHARACTERISTICS:										
248 GGCCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG 250 (2) INFORMATION FOR SEQ ID NO: 3: 252 (i) SEQUENCE CHARACTERISTICS:										
250 (2) INFORMATION FOR SEQ ID NO: 3: 252 (i) SEQUENCE CHARACTERISTICS:										
252 (i) SEQUENCE CHARACTERISTICS:										
253 (A) LENGTH: 2504 base pairs	253									
254 (B) TYPE: nucleic acid		•								

```
255
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear
256
258
        (ii) MOLECULE TYPE: DNA (genomic)
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
262
264 ATGGAGGCGA TGCTTCCGCT CTTTGAACCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC
                                                                            60
266 CACCTGGCCT ACCGCACCTT CTTCGCCCTG AAGGGCCTCA CCACGAGCCG GGGCGAACCG
                                                                           120
268 GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGTAC
                                                                           180
270 AAGGCCGTCT TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG
                                                                           240
272 GCCTACAAGG CGGGGAGGCC CCCGACCCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC
274 AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC
                                                                           360
276 GACGTTCTCG CCACCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC
                                                                           420
278 ACCGCCGACC GCGACCTCTA CCAACTCGTC TCCGACCGCG TCGCCGTCCT CCACCCCGAG
                                                                           480
                                                                           540
280 GGCCACCTCA TCACCCCGGA GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG
282 GTGGACTTCC GCGCCCTCGT GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC
                                                                           600
284 GGGGAGAAGA CCGCCCTCAA GCTCCTCAAG GAGTGGGGAA GCCTGGAAAA CCTCCTCAAG
                                                                           660
286 AACCTGGACC GGGTAAAGCC AGAAAACGTC CGGGAGAAGA TCAAGGCCCA CCTGGAAGAC
                                                                           720
288 CTCAGGCTCT CCTTGGAGCT CTCCCGGGTG CGCACCGACC TCCCCCTGGA GGTGGACCTC
290 GCCCAGGGGC GGGAGCCCGA CCGGGAGGGG CTTAGGGCCT TCCTGGAGAG GCTGGAGTTC
                                                                           840
292 GGCAGCCTCC TCCACGAGTT CGGCCTCCTG GAGGCCCCCG CCCCCTGGA GGAGGCCCCC
                                                                           900
294 TGGCCCCCGC CGGAAGGGGC CTTCGTGGGC TTCGTCCTCT CCCGCCCCGA GCCCATGTGG
                                                                           960
296 GCGGAGCTTA AAGCCCTGGC CGCCTGCAGG GACGGCCGGG TGCACCGGGC AGCAGACCCC
                                                                          1020
298 TTGGCGGGGC TAAAGGACCT CAAGGAGGTC CGGGGCCTCC TCGCCAAGGA CCTCGCCGTC
                                                                          1080
300 TTGGCCTCGA GGGAGGGGCT AGACCTCGTG CCCGGGGACG ACCCCATGCT CCTCGCCTAC
                                                                          1140
302 CTCCTGGACC CCTCCAACAC CACCCCGAG GGGGTGGCGC GGCGCTACGG GGGGGAGTGG
304 ACGGAGGACG CCGCCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA CCTCCTTAAG
                                                                          1260
306 CGCCTCGAGG GGGAGGAGAA GCTCCTTTGG CTCTACCACG AGGTGGAAAA GCCCCTCTCC
                                                                          1320
308 CGGGTCCTGG CCCACATGGA GGCCACCGGG GTACGGCTGG ACGTGGCCTA CCTTCAGGCC
                                                                          1380
310 CTTTCCCTGG AGCTTGCGGA GGAGATCCGC CGCCTCGAGG AGGAGGTCTT CCGCTTGGCG
                                                                          1440
312 GGCCACCCCT TCAACCTCAA CTCCCGGGAC CAGCTGGAAA GGGTGCTCTT TGACGAGCTT
                                                                          1500
314 AGGCTTCCCG CCTTGGGGAA GACGCAAAAG ACAGGCAAGC GCTCCACCAG CGCCGCGGTG
                                                                          1560
316 CTGGAGGCCC TACGGGAGGC CCACCCCATC GTGGAGAAGA TCCTCCAGCA CCGGGAGCTC
                                                                          1620
318 ACCAAGCTCA AGAACACCTA CGTGGACCCC CTCCCAAGCC TCGTCCACCC GAGGACGGGC
                                                                          1680
320 CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC
                                                                          1740
322 CCCAACCTGC AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CCGGGCCTTC
                                                                          1800
324 GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC
                                                                          1860
326 CTCGCCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC
                                                                          1920
328 CACACCCAGA CCGCAAGCTG GATGTTCGGC GTCCCCCCGG AGGCCGTGGA CCCCCTGATG
                                                                          1980
330 CGCCGGCCG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC
                                                                          2040
332 TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA
                                                                          2100
334 GCTTCCCCAA GGTGCGGCC TGGATAGAAA AGACCCTGGA GGAGGGAGG AAGCGGGGCT
                                                                          2160
336 ACGTGGAAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA
                                                                          2220
338 GCGTCAGGGA GGCCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG
                                                                          2280
340 ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCCGCCT CCGGGAGATG GGGGCCCGCA
                                                                          2340
342 TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG
                                                                          2400
344 TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG
                                                                          2460
                                                                          2504
346 TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG
348 (2) INFORMATION FOR SEQ ID NO: 4:
         (i) SEQUENCE CHARACTERISTICS:
350
351
              (A) LENGTH: 832 amino acids
```

352		(B	) TYI	PE: a	amino	o aci	id									
353																
354		•	•		GY: ]		_									
356	(ii)		•													
360		MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4:														
362	` '	_									Lvs	Glv	Arg	Val	Leu	Leu
363	1	**** 9	017	1100	5	110			014	10	-1-	V-1	5		15	
365		A cn	C117	wic	-	Leu	λla	Пагт	λνα		Dhe	Hic	Ala	T.e.11		Glv
	Val	АБР	GIY	20	nrs	пец	ALG	T A T	25	1111	riie	1113	AIG	30	טעט	OLY
366	T 011	Πh∽	Πh.~		7 ~~	C1 v	Clu	Dro		Cln	7 l s	V = 1	Tyr	-	Dhe	λla
368	ьeu	TIIT	35	ser	AIG	GTÄ	Giu	40	Val	GIII	AIA	vai	45	GLY	FIIC	пта
369	T	C		T	T	21-	T 011		C1	7 00	C1	7 00		370 ]	T1 A	17 a 1
371	ьуѕ		ьeu	ьeu	гуѕ	Ald		ьуѕ	GIU	Asp	GLY	60	Ala	Val	116	Vai
372		50			-		55	<b>a</b>	D1	3	77.2 -		27-	m	C1	c1
374		Pne	Asp	Ата	гаг		Pro	ser	Pne	Arg		GIU	Ala	TAT	GIY	
375	65	_			_	70	_	<b>—</b> 1	_	<b>a</b> 1	75	D1	D		<b>a</b> 1	80
377	Tyr	ьуs	АТА	GIĀ		Ата	Pro	Thr	Pro		Asp	Pne	Pro	Arg		ьeu
378		_		_	85	_		_	_	90	<b>6</b> 1	<b>.</b>			95	<b>a</b> 1
380	Ala	Leu	He		GLu	Leu	Val	Asp		Leu	GIĀ	Leu	Ala		Leu	GIU
381	_		_	100				_	105	_		_	_	110	_	_
383	Val	Pro		Tyr	Glu	Ala	Asp		Val	Leu	Ala	Ser	Leu	Ala	Lys	ьys
384			115					120		_			125		_	_
386	Ala	Glu	Lys	Glu	Gly	Tyr		Val	Arg	Ile	Leu		Ala	Asp	Lys	Asp
387		130					135					140				
389	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly
390	145					150					155					160
392	$\mathtt{Tyr}$	Leu	Ile	Thr		Ala	$\mathtt{Trp}$	Leu	${\tt Trp}$		Lys	Tyr	Gly	Leu		Pro
393					165					170					175	
395	Asp	Gln	$\mathtt{Trp}$	Ala	Asp	Tyr	Arg	Ala		Thr	Gly	Asp	Glu		Asp	Asn
396				180					185					190		
398	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu
399			195					200					205			
401	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu
402		210					215					220				
404	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys
405	225					230					235					240
407	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val
408					245					250					255	
410	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	Phe
411				260					265					270		
413	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu
414			275					280					285			
416	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly
417		290					295					300				
419	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	Asp
420	305					310					315					320
422	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Pro
423					325					330					335	
425	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	Leu
426				340					345					350		

Input Set : N:\Crf3\RULE60\10081806.raw
Output Set: N:\CRF3\07022002\J081806.raw

## Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the  $\langle 220 \rangle$  to  $\langle 223 \rangle$  fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 4,5,181,182,190,366,617,628,685,714,722,738,784,1022,1029
Seq#:7; N Pos. 1038,1053,1098,1105,1206,1227,1244,1251,1252,1253,1350,1380
Seq#:7; N Pos. 1497,1530,1569,1572,1641,1653,1655,1770,1812,2319,2346,2396
Seq#:8; Xaa Pos.2,63,109,186,205,209,227,228,233,240,243,244,247,260,290
Seq#:8; Xaa Pos.329,336,340,368,414,417,418,431,551,605,773,794,798,823,833
Seq#:57; N Pos. 18

VERIFICATION SUMMARY DATE: 07/02/2002
PATENT APPLICATION: US/10/081,806 TIME: 14:00:33

Input Set : N:\Crf3\RULE60\10081806.raw
Output Set: N:\CRF3\07022002\J081806.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:] L:974 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0 L:983 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:48 L:992 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:96 L:1007 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:176 L:1010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:192 L:1013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:208 L:1016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:224 L:1019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:240 L:1022 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:256 L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:288 L:1034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:320 L:1037 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:336 L:1040 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:352 L:1049 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:400 L:1052 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:416 L:1076 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:544 L:1085 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:592 L:1118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:768 L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:784 L:1127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:816 L:1130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:832 L:2269 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=56